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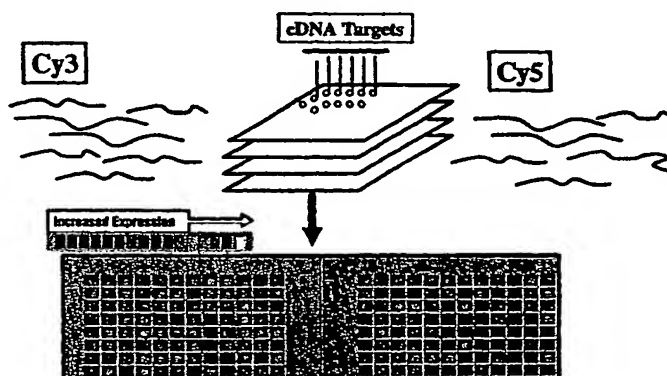
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[Continued on next page]

(54) Title: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY OF HEMATOLOGICAL MALIGNANCIES

Outline of Microarray Chip Technology approach



(57) Abstract: Disclosed are methods and compositions for the detection, diagnosis, prognosis, and therapy of hematological malignancies, and in particular, B cell leukemias, lymphomas and multiple myelomas. Disclosed are compositions, methods and kits for eliciting immune and T cell responses to specific malignancy-related antigenic polypeptides and antigenic polypeptide fragments thereof in an animal. Also disclosed are compositions and methods for use in the identification of cells and biological samples containing one or more hematological malignancy-related compositions, and methods for the detection and diagnosis of such diseases and affected cell types. Also disclosed are diagnostic and therapeutic kits, as well as methods for the diagnosis, therapy and/or prevention of a variety of leukemias and lymphomas.

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WO 03/062401 A2



TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Declarations under Rule 4.17:

- *as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii)) for the following designations AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW, ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent*

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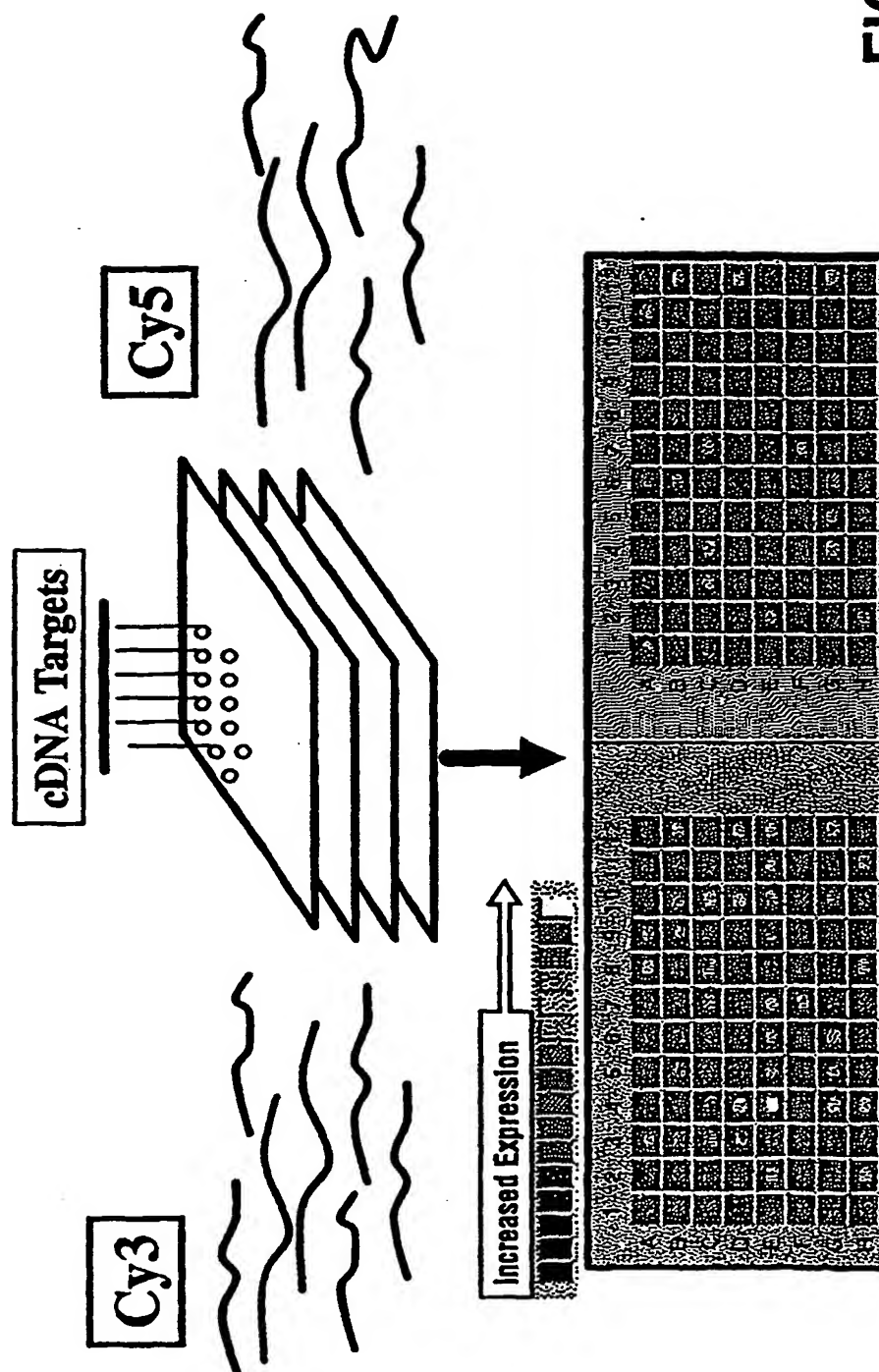
- *as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii)) for all designations*
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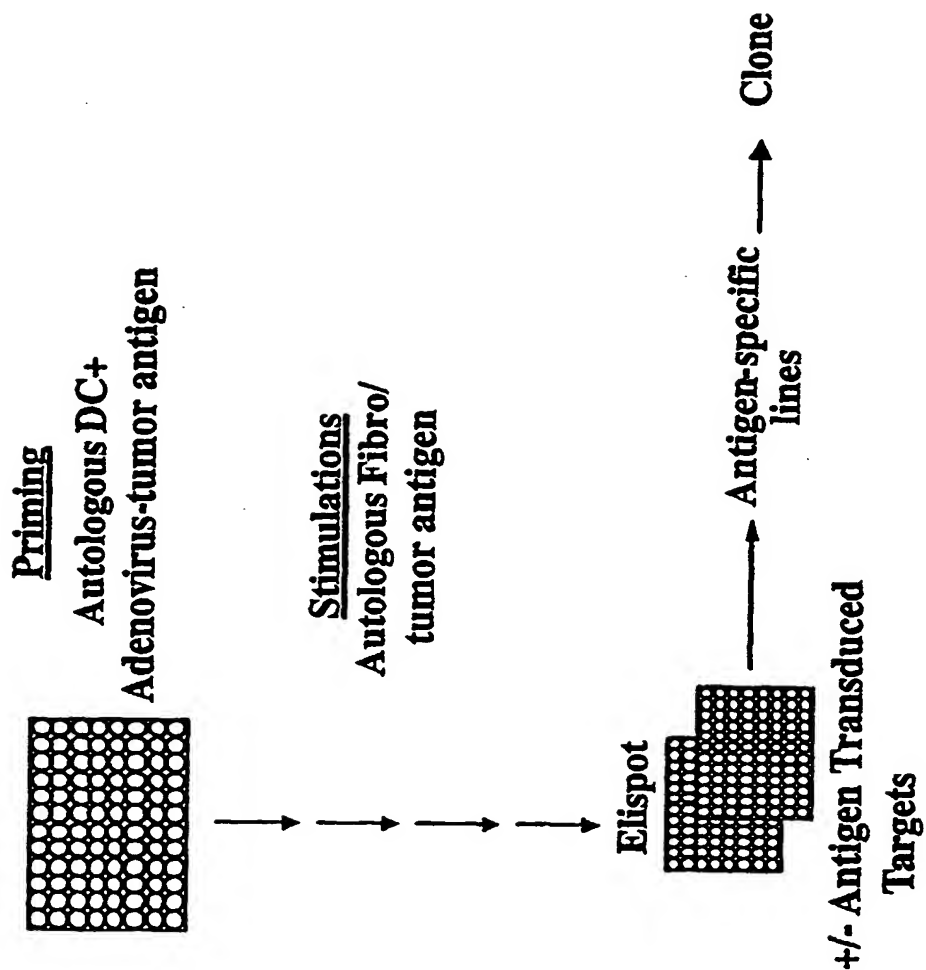
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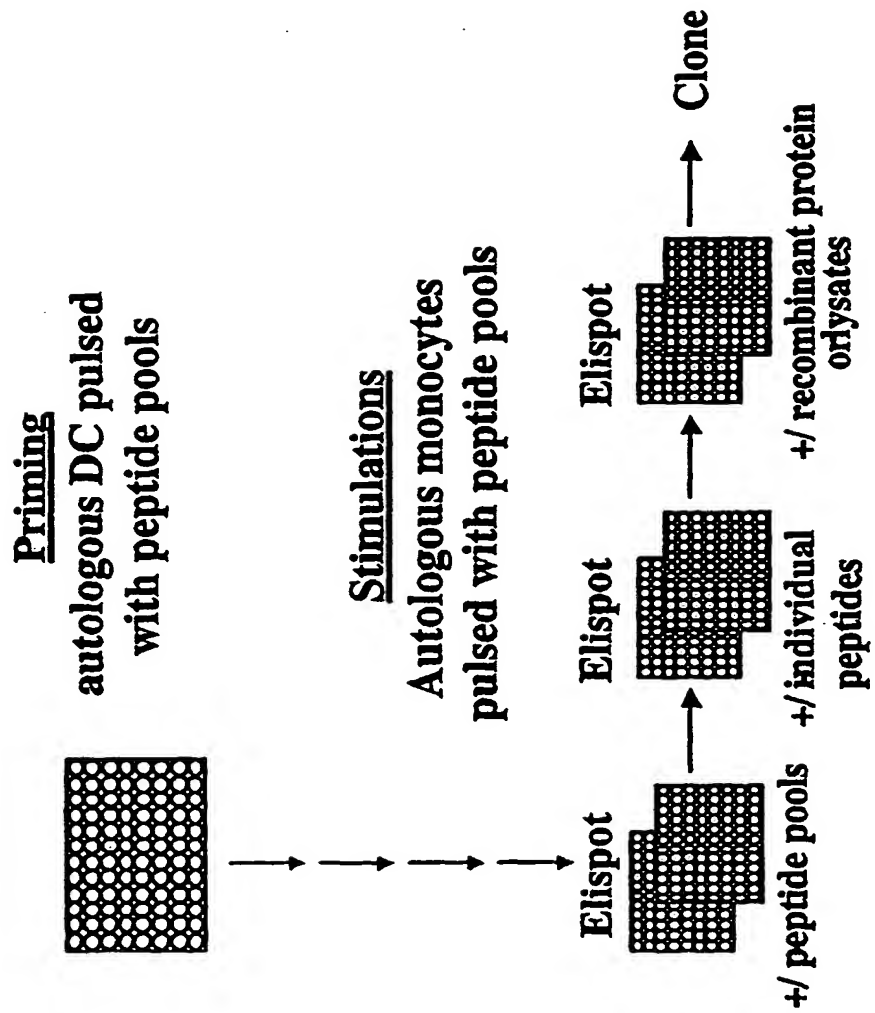
Outline of Microarray Chip Technology approach



General protocol for *in-vitro* whole gene CD8 T cell priming

**FIG. 2**

General protocol for *in-vitro* whole gene CD4 T cell priming

**FIG. 3**

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LEUKEMIA/LYMPHOMA CHIP #3: PROBES USED IN ANALYSIS

Cy3 Probe		Cy5 Probe	
Tissue	RNA#	RNA#	Tissue
Lymphoma, T cell	952	SPACT74	Kidney N
Lymphoma, B cell	955	SPACT81	Liver N
Lymphoma, B cell	953	SPACT78	Lung N
Lymphoma	916	SPACT42	Brain N
Lymphoma, Hodgkins	950	138598B	Skin N
Lymphoma, Hodgkins	950	SPACT49	Bone Marrow N
Lymphoma, B cell	CL151	888	PBMC resting
Lymphoma, T cell	904B	SPACT55	Stomach N
Lymphoma, Hodgkins see RNA 959	CL153	SPACT70	Thymus N
Lymphoma, B cell	CL152	SPACT75	Skeletal Muscle N
Lymphoma, B cell see RNA 958	CL155	SPACT73	Heart N
Lymphoma, B cell	944	243502B	Esophagus N
Lymphoma, B cell	958	1006	Colon N
Lymphoma, B cell	954	SPACT65	Small Intestine N
Lymphoma	960	779B	Trachea N
Lymphoma, T cell	957	S9327328	Bladder N
Lymphoma, B cell	914B		
Lymphoma, B cell	913		
Lymphoma, B cell	944B		
Lymphoma, B cell/failed	903		

GREEN: Tumor probes where gene expression would be desired.**RED:** Normal essential tissue probes where gene expression is to be avoided.**BLACK:** Normal tissue probes where gene expression is acceptable.**FIG. 4**

Hematology Therapeutic Ab Candidates

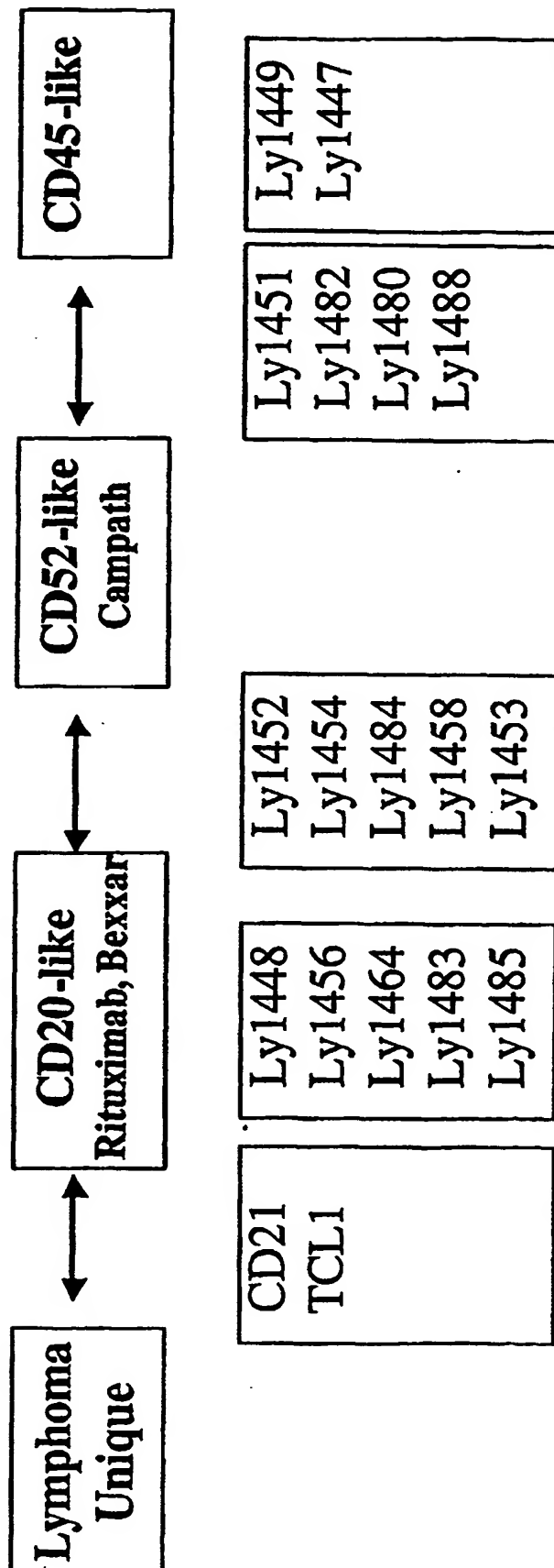


FIG. 5

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a. TMpred Report for Ly1484 Long**Date: 8/15/2001**

RDFQSEVLLSAMELFHMTSGGDAAMFRDGKEPQPSAEAAAAPSLANISCF
 TQKLVEKLYSGMFSADPREHLLFILEHMMVVEFTASSORDIVLSTLYSSL
 NKVILLYGLSKPQOQSLSECLGLLSILGLFLOEHWDVVFAT YNSNISFLLCLM
 HCLLLLNNERSYPEGFGLEPKPRMSTYHQVFLSPNEDVKEKREDLPSLSDV
 QHNIQKTVQTLWQQQLVAQRQQTLEDAFKIDLSVKPGEREVKIEEVTPLWE
 ETMLKAWQHYLASEKKS LASRSNVAHHSKVTLWSGSLSSAMKLMFGRQAK
 DPECKTEDFVSCIENYRRRGQELYASLYKDHVQRRKCGNIKAANAWARIQ
 EQLFGELGLWSQGEETKPCSPWELDWREGPARMRKRIKRLSPLEALSSGR
 HKESQDKNDHISQTNAENQDELTLREAEGERDEVGVDCTQLTFFPALHES
 LHSEDFLELCRERQVILQELLDKKVTQKFSLVIVQGHVSEGVLLFGHQ
 HFFYICENFELSPTEDEVYCHRHCLSNISDPFIDNLCSKDRSHDHYSQCHS
 YADMRELROARFLLQDIALLEIFFINGYSKFLV FYNNDRSKAFKSFCSFQP
 SLK GKATSEDTLNLRRYPGSDRIMLQKWQKRDISNFEYLMYLNNTAAGRTC
 NDYMQYPVFPWVLADYTSETLNLANPKIFRDLSKPMGAQT KERKLF IQR
 FKEVEKTEGDMTVQCHYYTHYSSAIIVASYLVRMPPTFOAFCALQ GCSFD
 VADRMFHSVKSTWESASRENMSDVRELEPPEFFYLPEFFLHNCNEVTEFCMQ
 DCFVLEDVQLPPWADEDPRKQFISLHRKALFESDFVSANLHHWIDLIFCYKQ
 QCPAAVDVAVNLTTHPYFYEDRMDLSSTLHDPLEKSTLLEFVSNTFCQVPKOLF
 TKQHPARTAAACKPLPKQDVSTFPVSLPCHPQPFYSLQSLRPSQVTVKDMY
 LFSLESESPKCATCHIVSTHKTPLAVERNKVLLPPLWNRTFSWCFDDFSC
 CLCSYCSDKVLMTHFENLAAWERCLCAVCPSPTHIVTSCHSTVVCVWELSM
 TKERPRELRLRQALYCHTQAVTCLAA SVTFSLVSGSODCTCTLWDLDEL
 THVTRLP AHREGTSALTTS DVSETHIVSCAGAHLSLWNVNCOPLASITFAW
 CPECATITCCCLMECPAWDTSQILITGSDCMVRVWKTFEDVKMSVPERPAC
 EEPLAOPPSPREHKWEKNLALSRRLDVSTALTEKPSKTS PAVFALAVSRN
 HFKLLVEDERERTFCWSADG (SEQ ID NO: 10,847)

Black = Intracellular, Red = Transmembrane,
 Blue = Extracellular

Ly1484 Long has 1269 amino acids and 5

Transmembrane Domains

Transmembrane Domain 1: 63 - 84	Score: 1.36675
Transmembrane Domain 2: 118 - 139	Score: 1.38695
Transmembrane Domain 3: 480 - 501	Score: 1.36185
Transmembrane Domain 4: 562 - 583	Score: 1.31785
Transmembrane Domain 5: 725 - 746	Score: 1.3521

FIG. 6

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b. TMpred Report for Ly1484 (short)**Date: 8/20/2001**

MLQKWQKRDISNFEYLMYLNNTAAGRTCNDYMQYPVFPWVLADYTSETLNL
 ANPKIFRDLSKPMGAQTKERKLKFIQRFKEVEKTEGDMTVQCHYYTHYSS
 AIIVASYLVRMPPFTQAFCALQCCSTFDVADRMFHSVKSTWESASRENMSD
 VREIHPPEFFYLPEFLTNCNEVEFCQMDCIFVLCDVOLPPWADGEDPRKFTS
 LHRKALESDSFVSANLHHWIDLITCEYKQOQCPAAVDVAVNIQHPYFYEDRMDL
 SSTTDPILTKSTILCFVSNFCQVPKQLFTKPHPARTAAACKPLPKDVDSTPV
 SLPGHPQPFYFYZLSLRPSQVTVKDMYLFSLCESSESPKCATGHVSTHKTI
 LAVERNKVLLPPLWNRHFSWGFDDFSCCLCSYCESDKVLMHFFENLAAWERC
 LCAVCPSPHTIVISGISTVVCWELSMFKERPRGLRLRQALYGHQAVTC
 LAASVHFSLHVSQSDCTCITLWDLHDHHTHVTRLPAHREGTSATHTSDVSG
 TIVSCAGAILSLWNVNGOPLASTTAWCEPACATCCGLMECPAWDTSQIT
 ITESQDCMVRVWKTHDVKMSVPCRRAGEEPLAOPPSPRCHKWEKNLALSR
 ELDVSTALTEKPSKTSPTAVTALAVSRNHTEKLLVEDERGRITFCWSADG

(SEQ ID NO: 10,848)

Black = Intracellular, Red = Transmembrane,**Blue = Extracellular**

**Ly1484 has 646 amino acids and 1 Transmembrane
 Domains**

Transmembrane Domain 1: 102 - 123

Score: 1.3521

FIG. 6 (cont.)

ANALYSIS RESULTS OF THE PROGRAM TSITES.

Mon, Aug 27, 2001 11:29:26 AM

These are the results of the analysis of the file--> LY1484~1.TXT

Beginning with residue: 1 and ending with residue: 1270

AMPHI Window size: 11

A-AMPHI mid points of blocks.

R-Residues matching the Rothbard/Taylor motif.

D-Residues matching the IAd motif.

d-Residues matching the IEd motif.

(SEQ ID NO: 10,847)

5	10	15	20	25	30	35	40	45	50	55	60	65	70	75	8/15
RDFQSEVLLS	AMELFHMT	SGGDAAM	FRDCKE	PPQPSAE	AAAPSL	ANISCF	TQKLVE	KLYSGM	FSADPR	HILLFIL					

.....AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
.....RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
.....DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

80	85	90	95	100	105	110	115	120	125	130	135	140	145	150	
EHIMV	VIETAS	SQRD	TVLST	LYSS	LNVIL	CLSK	PQQL	SECL	GLLS	ILGFL	QEHWD	VVFAT	YNSN	ISFL	CLIM
.....AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
.....RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
.....DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

FIG. 7

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155 160 165 170 175 180 185 190 195 200 205 210 215 220 225
HCLLLNERSYPEGFGLEPKPRMSTYHQVFLSPNEDVKEKREDLPSLSDVQHNIOKTQTLWQQLVAQRQQTLED
.....AAAA.AAAAA.AAAAAA.....
.....RRRR.....R
.....
.....

230 235 240 245 250 255 260 265 270 275 280 285 290 295 300
AFKIDLSVKPGEREVKIEEVTPLWEETMLKAWQHLYLASEKKSLASRSNVAHHSKVTLWSGSLSSAMKLMPCRQAK
.....AAA...AAAAAA.....AAAAAA
RRR.....RRRRRRRRRR.....RRRR.....
.....
.....ddd.....

305 310 315 320 325 330 335 340 345 350 355 360 365 370 375
DPECKTEFVSCIENYRRRGQELYASLYKDHVQRRKCGNIKAANAWARIQEQLFGELGLWSQGEETKPCSPWELD
.....AAAAAA.....AAAAAA.AAAAA.AAA.....
.....RRRR.....RRRR.....RRRR.....
.....
.....

380 385 390 395 400 405 410 415 420 425 430 435 440 445 450
WREGPARMRKRIKRLSPLEALSSGRHKESQKNDHISQTNQDELTLREAEGEPEVGVDTQTLTFFPALHES
.....AAAA.AAAAA.AAAAAA.....AAAA.AAAA.
.....RRRR.....RRRR.....
.....DDDDDD.....
.....ddd.....

FIG. 7 (cont.)

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```

455 460 465 470 475 480 485 490 495 500 505 510 515 520 525
LLHSEDFLELCRERQVILQELLDKEKVTQKFSLVIVQGHLVSEGVLFFGHQHFYICENFTLSPTGVDVCTRHCLSN
      AAAA.....RRRR.RRRR.....AAAA
      RRRR.....RRRR.....RRRR.....RRRR.....RRRR.....RRRR.....RRRR.....RRRR.....

```

```

530 535 540 545 550 555 560 565 570 575 580 585 590 595 600
IISDPFIFNLCSKDRSTDHYSCQCHSYADMRELQARFLQDIALEIFFHNGYSKFLVFYNNDRSKAFKSFCSFQP
A.AAAAAA.....AAAAA.....AAAAA.....AAAAA.....
.....RRRRRRRRRRRR.....RRRR.....
.....
.....
.....

```

```
605 610 615 620 625 630 635 640 645 650 655 660 665 670 675
SLK GKATSEDTLNLRRYPGSDRIMLQKWQKRDISNFEYLMYLNTAAGRTCNDYMQVPFVWLADYTSETLNLAN
.....AAAAA.....AAA.....AAAAAAAAA.....RRRRRRRR...
DDDDDD.....
```

680 685 690 695 700 705 710 715 720 725 730 735 740 745 750
PKIFRDLSPMGAOTKERKLFIOFKEVEKTEGDMTVQCHYYTHYSSAIIVASLYVRMPFFTQAFCALQGGSFD
AAAAAAAAAAAAA.....AAAAAAAAAAAA.....AAAAA.....
RRRR.....RRRR.....RRRR.RRRRR.....RRRR.....RRRR.....RRRR.....RRRR.....

FIG. 7 (cont.)

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..... DDDDDDDDDDD.....
..... dddd.....
755 760 765 770 775 780 785 790 795 800 805 810 815 820 825
VADRMFHSVKSTWESASRENMSDVRELTPPEFFYLPEFLTNCNGVEFGCMODGTVLGDVQLPPWADGDPKRFISLH
AAAAAAAAAAAA.AA.AAAA.AAAAAA.....AAA.....
RRRRRRR.....RRRRR.....RRRRR.....RRRR.....
.....
.....
830 835 840 845 850 855 860 865 870 875 880 885 890 895 900
RKALESDFVSANLHHWIDLIFGYKQOGPAAVDAVNIFHPYFYGDRMDLSSITDPLIKSTILGFVSNFGQVPKQLF
.....AAAAAAA.....AAAAAAA.....AAAAA.AAAAAA.AAAAAA.AAAAAA
.RRRR.RRRR.....RRRR.....RRRR.....RRRR.....
.....DDDDDD.....
.....
905 910 915 920 925 930 935 940 945 950 955 960 965 970 975
TKPHPARTAAGKPLPGKDVSTPVSLLPGHPQPFYSLQSLRPSQVTVKDMYLFSLGSESPKGAIGHIVSTEKTLA
.....AAAAAAA.....AAAAA.....
.....RRRR.....RRRRRRR.....
.....DDDDDD.....DDDDDD.....
.....

FIG. 7 (cont.)

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980 985 990 995 1000 1000 1010 1015 1020 1025 1030 1030 1040 1045 1050
VERNKVLLPPLWNRFTFSWGFDDFSCCLGSYGSDKVLMTFENLAWGRCLCAVCPSTTIVTSGTSTVVCWELSM
.....AAAAA.....
.....RRRR.....
.....DDDDDDDDDD.....
.....
1055 1060 1065 1070 1075 1080 1085 1090 1095 1100 1105 1110 1115 1120 1125
TKGRPRGLRLRQALYGHQAASVTFSLLVSGSDCTCILWLDHLTHVTRLPAHREGISAITISDVSGTI
.....AAAAA.....
.....RRRRRR.....
DDD...DDDDDDDDDD.....
.ddddd.
1130 1135 1140 1145 1150 1155 1160 1165 1170 1175 1180 1185 1190 1195 1200
VSCAGAHLSLWNVNGOPLASITTAWGPEGAITCCCLMEGPAWDTSQIIITGSQDGMVRVWKTEDVKMSVPGRPAG
A.....AAA.....AAAAA.....
RR.....RRRR.....
D.....DDDDDD.....
.....
1205 1210 1215 1220 1225 1230 1235 1240 1245 1250 1255 1260 1265 1270 1275
EEPLAQPPSPRGHKWEKNLALSRELDVSIALTGKPSKTSPAVTALAVSRNHTKLLVGDERGRIFCWSADG
.....
.....RRRR.....
.....DDDDDDDD.....
.....

FIG. 7 (cont.)

FIG. 8

ANALYSIS RESULTS OF THE PROGRAM TSITES.

Mon, Aug 27, 2001 10:34:51 AM

These are the results of the analysis of the file--> LY1484~2.TXT
Beginning with residue: 1 and ending with residue: 647
AMPHI Window size: 11

A-AMPHI mid points of blocks.

R-Residues matching the Rothbard/Taylor motif.

D-Residues matching the IAD motif.

2-Residues matching the IED motif.

QID NO:

```
[0,848) 5   10   15   20   25   30   35   40   45   50   55   60   65   70   75
MLQKWQRDISNFEYLMYLNTAAGRTCNDYMQYPVPWVLADYTSETLNLANPKIFRDLSPMGATKERRQLKFI
...AAA.....AAAAA....AAAAAAAA..AAA
...RRRR.....RRRRRRR.....RRR.....RRR
...ddddd.....
```

[illegible]

```

155   160   165   170   175   180   185   190   195   200   205   210   215   220   225
VRELTPEFFYLPFLTNCNGVEFGCMQDGTVLGDVQLPPWADGDPKFFISLHRKALESDFVSANLHHWIDLIFGY
AAAAA.....AAAAAA..AAA.....RRRRR.RRRR...AAAAA....
..RRRRR...RRRRR.....RRRRR.....RRRRR.RRRR...RRRRRRRR.
.....
```

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[illegible]

FIG. 8 (cont.)


```

530 535 540 545 550 555 560 565 570 575 580 585 590 595 600
AWGPEGAITCCCLMEGPAWDTSQIIITGSQDGMVRVWKTEDVKMSVPGRPAGEEPLAQPPSPRGHKWEKNLALSR
.....AAAAAAA.....
.....RRRR.....RRRRRR.....
D.....DDDDDD..DDDDDD.....
.....
605 610 615 620 625 630 635 640 645 650 655 660 665 670 675
ELDVSIALTGPKSPTSPAVTALAVSRNHTKLLVGDERGRIFCWSADG
.....RRRR.....
.DDDDDDDDD.....DDDDDDDD..dddddd.....
.....

```

FIG. 8 (cont.)

INFORMAL SEQUENCE LISTING

<210> 1
<212> DNA
<213> Homo sapiens

<400> 1

1>Ly1728P, membrane protein FOAP-12, full-length cDNA
cttcagagagcaatatggctggttccccaacatgcctcaccctcatctatcctttggcagctcacag
ggtcagcagcctctggaccctgtaagagctgggtcggttccggttggtggggccgtgactttccccctgaa
gtccaaagtaaaagcaagttgactctattgtctggaccttcaacacaaccctcttgtcaccatacagcca
gaagggggcactatcatagtgacccaaaatcgtaatatgggagagagtagacttcccagatggaggctact
cctgaagctcagcaaaactgaagaagaatgactcagggatctactatgtggggatatacagctcatcact
ccagcagccctccacccaggagtagctgctgcatgtctacgagcacctgtcaaagcctaaagtaccatg
ggtctgcagagcaataagaatggcacctgtgtgaccaatctgacatgtcgtcatggaacatggggaagagg
atgtgatttatacctggaaggccctggggcaagcagcaatgagtcaccataatgggtccatcctccccat
ctcctggagatggggagaaagtgtatgaccttcatctgctgtgcccaggaaacctgtcagcagaaacttc
tcaagccccatccttgcccaggagctctgtgaagggtgctgctgatgacccagattcctccatgggtccctcc
tgtgtctcctgttgggtgcccctcctgctcagctctcttctgactggggctatttctttggtttctgaagag
agagagacaagaagagtacattgaagagaagaagagagtggaacatttctcgggaaactcctaacaatagc
ccccattctggagagaacacagagtacgacacaatccctcacactaatagaacaatcctaaggaagatc
cagcaaatcacggtttactccactgtggaaataccgaaaaagatggaaaaatccccactcactgctcacgat
gccagacacaccaaggctatttgcctatgagaatgttatctagacagcagtgactcccctaagtctctg
ctcaaaaaaaaaaacaattctcgccccaaagaaaacaatcagaagaattcactgatttgactagaacaatc
aaggaagaatgaagaacgttgactttttccaggataaattatctctgatgcttctttagatttaagagt
tcataattccatccactgctgagaaatctcctcaaacccagaaggtttaatcacttcatccaaaaatgg
gattgtgaatgtcagcaaacataaaaaaagtgtcttagaagattcctatagaatgtaaatgcaagggtc
acacataattaatgacagcctgtgtattaatgatgggtccagggtcagtgctgagggtttcattccatccc
agggcttggtatgtaaggattataccaagagctctgctaccaggagggtcaagaagaccaaacagacagac
aagtcacagcagaagcagatgcacctgacaaaaatggatgtattaattgggtctataaaactatgtgcccag
cactatgctgagcttacactaattgggtcagacgtgctgctgcccctcatgaaattgggtccaaatgaatg
aactactttcatgagcagttgttagcaggcctgaccacagattcccagagggccagggtgtggatccacagg
acttgaagggtcaaagttcacaaagatgaagaatcagggttagctgacctgtttggcagatactataatgg
agacacagaagtgctgcatggcccaaggacaaggacctccagccagggttcatttatgcacttgtgctgca
aaagaaaagtctagggttttaagggtgtgcccagaacccatcccaataaagagaccgagcttgaagtcacat
tgtaaatctagtgtaggagacttggagtcaggcagtgagactggtggggcagggggcagtggggtact
gtaaaccttttaagatgggttaattcattcaatagatatttatttaagaacctatgcggcccgcatgggtgg
ctcacacctgtaatcccagcactttgggaggccaagggtgggtgggtcatctgaggtcaggagttcaagac
cagcctggccaacatgggtgaaacccccatctctactaaagatacaaaaaatttgctgagcgtgggtgggtg
acctgtaatcccagctactcgagaggccaaggcatgagaatcgcttgaacctgggaggtggaggttgag
tgagctgagatggcaccactgcactccggcctaggcaacgagagcaaaactccaatacaaaacaaacaaac
aaacacctgtgctagggtcagtcctggcagctaagatgaacatccctaccaacacagagctcaccatctctt
atacttaagtgaaaaaacatgggggaaggggaaggggaatgggtgcttttgatatgttccctgacacatat
cttgaatggagacctccctaccaagtgatgaaagtgtgaaaaacttaataacaaatgcttgggtgggcaa
gaatgggattgaggattatctctctcagaaaggcattgtgaaggaattgagccagatctctctccctac
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aaaaaaaaaaaa

<210> 2
<212> PRT
<213> Homo sapiens

<400> 2

2>Ly1728P, FOAP-12, full-length protein
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IVTQNRNRERVDFFPDGGYSLKLSKLKKNDSGIYVVGIIYSSSLQQPSTQEYVLHVYEHLSKPKVTMGLQSN
KNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWGESDMTFICVARNPVSRNFSSPIL
ARKLCEGAADDPDSSMVLCLLLVPLLLSLFVLGLFLWFLKREKQEEYIEKKRVDICRETPNICPHSGE
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<210> 3
<212> DNA
<213> Homo sapiens

<400> 3

3>Ly1732P, BCM, full-length cDNA

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<210> 4
 <212> PRT
 <213> Homo sapiens
 <400> 4

4>Ly1732P, BCM, full-length protein
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<210> 5
 <212> DNA
 <213> Homo sapiens
 <400> 5

5>Ly1888P, anti-Fas-induced apoptosis (TOSO), full-length cDNA
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<210> 6
 <212> PRT
 <213> Homo sapiens
 <400> 6

6>Ly1888P, anti-Fas-induced apoptosis (TOSO), full-length protein
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 WFHLPLYLFQMPAYASSSKFVTRVTTPAQRGKVPVHHSSPTTQITHRPRVSRASSVAGDKPRTFLPSTTA
 SKISALEGLLPQTPSYNHTRLHRQRALDYGSQSGREGQGFHILIPTILGLFLLALLGLVVKRAVERRK
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<210> 7
<212> DNA
<213> Homo sapiens

<400> 7

7>Ly1452_His-tag-fusion, Old-SEQ-ID_10482, full-length cDNA
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<210> 8
<212> PRT
<213> Homo sapiens

<400> 8

8>Ly1452_His-tag-fusion, Old-SEQ-ID_10483, full-length protein
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LESVASAAT

<210> 9
<212> DNA
<213> Homo sapiens

<400> 9

9>Ly1452P_LS_400351.4_Edited, splice-1, full-length cDNA

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<210> 10

<212> PRT

<213> Homo sapiens

<400> 10

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<210> 11

<212> DNA
<213> Homo sapiens

<400> 11

11>Ly1452P, splice-2, FLJ21562, full-length cDNA

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<210> 12
<212> PRT
<213> Homo sapiens

<400> 12

12>Ly1452P, splice-form-2, FLJ21562, full-length protein

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<210> 13
<212> DNA
<213> Homo sapiens

<400> 13

13>Lyl1462P, Old-SEQ-ID_6411, partial cDNA

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<210> 14

<212> DNA

<213> Homo sapiens

<400> 14

14>Lyl1462P, Human Epstein-Barr virus complement receptor type II(cr2)_full-length

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<210> 15

<212> PRT

<213> Homo sapiens

<400> 15

15>Lyl1462P, CR2/CD21/C3d/Epstein-Barr virus receptor, full-length
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<210> 16

<212> DNA

<213> Homo sapiens

<400> 16

16>Lyl1484P, Old-SEQ-ID_10493, partial cDNA
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<210> 17

<212> DNA

<213> Homo sapiens

<400> 17

17>Lyl1484P, KIAA1607, full-length cDNA
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<210> 18

<212> PRT

<213> Homo sapiens

<400> 18

18>Lyl484P, KIAA1607, full-length protein

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<210> 19

<212> DNA

<213> Homo sapiens

<400> 19

19>Lyl1486P, Old-SEQ-ID_5058, partial cDNA

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<210> 20

<212> DNA

<213> Homo sapiens

<400> 20

20>Lyl1486P, Fc fragment of IgE, low affinity II, receptor for (CD23A), full-length

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<210> 21
<212> PRT
<213> Homo sapiens

<400> 21

21>Ly1486P, Fc fragment of IgE, low affinity II, receptor for (CD23A)_full-length
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LREEVTKLRMELQVSSGFVNCNTPCEKWINFORQCYFFGKGTQVHARYACDDMEGQLVSIHSPPEQDFL
TKHASHTGSWIGLRNLDLKGFEIWDGSHVDYSNAPGEPTSRSQGEDCVMRSGRWNDAFCDRKLGAW
VCDRLATCTPPASEGSAESMGPSRDPDPDGLRTPSAPLHS

<210> 22
<212> DNA
<213> Homo sapiens

<400> 22

22>Ly1677P, novel, partial, cDNA
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<213> Homo sapiens

<400> 23

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<212> DNA
<213> Homo sapiens

<400> 24

24>Ly1693P, Old-SEQ-ID_2611, partial cDNA
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<210> 25

<212> DNA

<213> Homo sapiens

<400> 25

25>Ly1693P, CXCR4, full-length cDNA

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<210> 26

<212> PRT

<213> Homo sapiens

<400> 26

26>Lyl1693P, CXCR4, full-length protein

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<210> 27

<212> DNA

<213> Homo sapiens

<400> 27

27>Lyl1697P, novel, partial cDNA

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<210> 28

<212> DNA

<213> Homo sapiens

<400> 28

28>Lyl1715P, lectin-like NK cell receptor (LTL1), full-length cDNA

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<210> 29

<212> PRT

<213> Homo sapiens

<400> 29

29>Ly1715P, lectin-like NK cell receptor, full-length protein
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<210> 30

<212> DNA

<213> Homo sapiens

<400> 30

30>Ly1727P, Old-SEQ-ID_6042, partial cDNA
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<210> 31

<212> DNA

<213> Homo sapiens

<400> 31

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<210> 32
<212> PRT
<213> Homo sapiens

<400> 32

32>Ly1727P, pim-2 proto-oncogene homolog pim-2h, full-length protein
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WSPLSDSVTCPLEVALLWKVGAGGGHGPVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPS
RCFFGQVVAAIQHCHSRGVVHRDIKDENILIDLRRGCAKLIDFGSGALLHDEPYTFDGTTRVYSPPEWIS
RHQYHALPATVWSLGIILYDMVCGDIPFERDQEI LEAELHFP AHVSPDCCALIRRCLAPKPSRRPSLEEI
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<210> 33
<212> DNA
<213> Homo sapiens

<400> 33

33>Ly1885P_DKFZp564F112 (from clone DKFZp564F112)_partial cDNA
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<210> 34
<212> DNA
<213> Homo sapiens

<400> 34

34>Ly1885P, CCP8 mRNA, full-length cDNA
tcctctttccgtgcgcgagtgacacagctccggaggcccgagccgaccctggggcggtccgggtccgggtgggtc
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<210> 35

<212> DNA

<213> Homo sapiens

<400> 35

35>Ly1885P, CCP8, full-length protein

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 TAYPALEETSTIEAEQKIPEDSIYIGTASDDSDIVTLEPPKLEEIGNQEVVIVEEAQSSSEDFNMGSSS
 SSQYTFQCPETVFSSQPSDDSSDETSTNQPSAPFRRRRARKKTVSASESEDRLVAEQETEPSKELSKRQ
 FSSGLNKCIVILALVIAISMGFGHYGTIIQIKRQQLVRKIHEDELNDMKDYLSQCQEQESFIDYKSLKE
 NLARCWTLTEAEKMSFETQKTNLATENQYLRLVSLEKEEKALSSLQEELNKLREQIRILEDKGTSTELVKE
 NQKLKQHLEEEKQKKHSFSLQRETLTLEAKMLKRELERERLVTALRGELQQLSGSQLHGKSDSPNVYTE
 KKEIAILRERLTLEKRLTFEQQRSDLWERLYVEAKDQNGKQGTGDKKKGGGRGSHRAKNKSKETFLGSVK
 EPTFDAMKNSTKEFVRHHKEKIKQAKEAVKENLKKFSDSVKSTFRHFKDITKNI FDEKGNKRFGATKEAAE
 KRPTVFDYLYHPQYKAPTENHSRPPYAKRWKEKPVHFKEFRKNTNSKKCSPGHDCRENSHSFRKACSGV
 FDCAQQESMSLFTNTVPIPIRMDEFRIIQRMYLKELDTCRWNELDQFINKFFLNGVFIHDQKLFTDFVN
 DVKIIILGNMKEYEVDNDGVFEKLDEYIYRHFFGHTFSPPYGPRSVYIKPCHYSSL

<210> 36

<212> DNA

<213> Homo sapiens

<400> 36

36>Ly1905P_Old-SEQ-ID_546, partial cDNA

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<400> 37

<400> 38

<400> 39

17/49

<212> PRT
<213> Homo sapiens

<400> 40

40>Ly1905P pim-2 oncogene full-length
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WSPLSDSVTCPLEVALLWKVAGGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPS
RCFFGQVVAAIQHCHSRGVVHRDIKDENILIDLRRGCAKLIDFGSGALLHDEPYTDFDGRVYSPPEWIS
RHQYHALPATVWSLIGILLYDMVCGDIPFERDQEI LEAELHFP AHVSPDCCALIRRCLAPKPSSRPSLEEI
LLDPWMQTPAEDVPLNPSKGGPAPLAWSLLP

<210> 41
<212> DNA
<213> Homo sapiens

<400> 41

41>Ly663S_Old_SEQ-ID_2757 partial cDNA
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cttttggtggttttctctacnacntcccgaagcttcntccag

<210> 42
<212> DNA
<213> Homo sapiens

<400> 42

42>Ly663S CD37 antigen (CD37) full-length cDNA
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cccaggagagctgcctcagcctcatcaagtacttctcttcggtttcaacctcttcttctcgtcctcgg
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cctac

<210> 43
<212> PRT
<213> Homo sapiens

<400> 43

43>Ly663S, CD37 antigen, full-length
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IALLGCVGALKELRCLLGLYFGMLLLLFATQITLILISTORAQLERSLRDVVEKTIQKYGTNPETA AE
ESWDYVQFQLRCCGWHYPQDWFQVLILRNGNSEAHRVPCSCYNLSATNDSTILDKVILPQLSRLGHLARS
RHSADICAVPAESHIYREGCAQLQKWLHNNLISIVGICLGVGLLELGFMTLSIFLCRNLDHVYNRLARY
R

<210> 44
<212> DNA
<213> Homo sapiens

<400> 44

44>Ly664S, FLJ90810 fis, clone weakly similar to PROTEIN DISULFIDE ISOMERASE-
RELATED PROTEIN PRECURSOR, full-length

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<210> 45

<212> PRT

<213> Homo sapiens

<400> 45

45>Ly664S, full-length

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FTHGIQSAAHFVMPFAPWCGHQRLOPTWNLGDKYNSMEDAKVYVAKVDCTAHSDVCSAQGVRYPTLK
LFPKPGQEAUVKYQGPDRDFQTLNWMLOTLNEEPVTPPEPEVEPPSAPELKQGLYELSSNFELHVAQGDHFI
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HRFVLSQAKDEL

<210> 46

<212> DNA

<213> Homo sapiens

<400> 46

46>Ly667S, Old-SEQ-ID_9413, partial cDNA

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accaccttct

<210> 47

<212> DNA

<213> Homo sapiens

<400> 47

47>Ly667S, Semaphorin B, full-length

aggatgatgaaagtgagaccgtcttagggcccttccagatagtgaaaccttctctgccccaatgccccacc
cctgcccacatacacacgcttctgtgctggggcttctctattgggtcctcgggggagtggtgtaagaa
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<210> 48

<212> PRT

<213> Homo sapiens

<400> 48

48>Ly667S, Semaphorin B, full-length

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GDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLY
TCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTAVLVDGMLYSGTMNNFLGSEPIILMR
TLGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQ
KKWTTFLKAQLLSAPSRGSCPSTSSATRSCSPPILPQLPTSTQSSPPSGQVGGTRSSAVCAFSLLDIERV
FKGKFKELNKETSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLA
VETAQGLDGHSHLVMYLGTTTGSLSLHKAVVSGDSSAHLVEEIQLPDPEPVRNLQLAPTQGAFFVGFSGGV
WRVPRANCSEYSCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRPQ
SRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPEASSTVYNGSLLLIVQDGVGGGLYQCWATEN
GFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQSYWPHFVTVTVLFAVLVLSGAL
IILVASPLRLRLRARGKVQGCETLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA

<210> 49

<212> DNA

<213> Homo sapiens

<400> 49

49>Ly677S, Old-SEQ-ID_465, partial cDNA

accagcagtcctgcggcacctacctccgcgtgcgccagccgccccccagggcccttcctgg
acatgggggagggcaccaagaacccaatcatcacagccgaggggatcatcctcctgttct
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gg

<210> 50

<212> PRT

<213> Homo sapiens

<400> 50

50>Ly677S, Old-SEQ-ID_1923, partial protein

QQSCGTYLRVRQPPRPFLDMGEGTKNRIITAEGIIILLFCAVVPGTLLLRKRWQERXLX

<210> 51

<212> DNA

<213> Homo sapiens

<400> 51

51>Ly677S, Old-SEQ-ID_5989, partial cDNA

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gg

<210> 52

<212> PRT

<213> Homo sapiens

<400> 52

52>Ly677S, Old-SEQ-ID_1496, partial protein

QQSCGTYLRVRQPPRPFLDMGEGTKNRIITAEGIIILLFCAVVPGTLLLRKRWQERXLX

<210> 53

<212> DNA

<213> Homo sapiens

<400> 53

53>Ly677S, CD79A antigen (immunoglobulin-associated alpha), full-length

tgctgcaactcaaactaaccaaccactgggagaagatgcctgggggtccaggagtcctccaagctctgc
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<210> 54
<212> PRT
<213> Homo sapiens

<400> 54

54>Ly677S, CD79A antigen, complete protein
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HGNYTWPFELGPGEDPNGTLIIQNVNKS HGGIYVCRVQEGNESYQQSCGTYLRVRQPPRPFLDMGEGT
KNRIITAEGLIILFCVAVPGTLLLFKRWQNEKLGLDAGDEYEDENLYEGLNLDDCSMYEDI SRGLQGT
QDVGSLNIGDVQLEKP

<210> 55
<212> DNA
<213> Homo sapiens

<400> 55

55>Ly1891P, orphan G-protein coupled receptor (GPCR5D), full-length
atgtacaaggactgcacgagtcactggagactatcttctctgtgacgccgaggggcatggggca
tcattctggagtccttggccatacttggcatcgtggtcacaattctgtactcttagcatttctcttct
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<210> 56
<212> PRT
<213> Homo sapiens

<400> 56

56>Ly1891P, orphan G-protein coupled receptor (GPCR5D), full-length
MYKDCIESTGDYFLLCDAEGPWGIIIESLAIIIGIVVTIILLLAFILMRKIQDCSQWNVLPTQLLFLLSV
LGLFGLAFAFIIELNQQTAPVRYFLFGLFALCFSCLLAHASNLVKLVRCVSFSWTTILCIAIGCSLLQ
IIIIATEYVTLIMTRGMFMFVNMTPCQLNVDFVLLVYVFLMALTFVSKATFCGPCENWKQHGRLI FITV
LFSIIIIWVWISMLLRGNPQFORQPQWDDPVVCIALVTNAWVFLLYIVPELCILYRSCRQECPLQGNAC
PVTAYQHSFQVENQELSRARDSGAEEDVALTSYGTPIQPQTVDPDTPQECFIPQAKLS PQDAGGV

<210> 57
<212> DNA
<213> Homo sapiens

<400> 57

57>CD138, syndecan 1 (SDC1), full-length cDNA
ggcacgaggaagggcctgtgggtttattataaggcggagctcggcgggagaggtgcgggccgaatccgag

ccgagcggagaggaatccggcagtagagagcggactccagccggcggaccctgcagccctcgccctgggac
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taagta

<210> 58
<212> PRT
<213> Homo sapiens

<400> 58

58>CD138, syndecan 1 (SDC1), full-length protein
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LTAIPTSPPEPTGLEATAASTSTLPAGEGPKGEAVVLPEVEPGLTAREQEATPRPRETTQLPTTHQASTT
TATTAQEPATSHPHRDMQPGHHETSTPAGPSQADLHTPHTEDGGPSATERAAEDGASSQLPAAEGSGEQD
FTFETSGENTAVVAVEPDRRNQSPVDQATGASQGLLDRKEVLGGVIAVGLVGLIFAVCLVGFMLYRMKK
KDEGSYSLEEPKQANGGAYQKPTKQEEFYA

<210> 59
<212> DNA
<213> Homo sapiens

<400> 59

59>CD22, Old-SEQ-ID_4021, partial cDNA
ctggggctgaggatggaggtccaagactgagaaatggatggaacgaatacacctcaatgtc
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<210> 60
<212> DNA
<213> Homo sapiens

<400> 60

60>CD22, full-length cDNA

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aataaaaatggctcagatgccacttcaagaaaaa

<210> 61

<212> PRT

<213> Homo sapiens

<400> 61

61>CD22, full-length protein

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FDGTRLYESTKDGKVPSEQKRQVFLGDKNKNCTLSIHPVHLNDSGQLGLRMESKTEKWMERIHLNVSERP
FPPHIQLPPEIQESQEVTLTCLLNFSYGYPIQLQLWLEGVPMRQAAVTSTSLTIKSVFTRSELKFSQW
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KDGTSLKKQNTFTLNLREVTKDQSGKYCCQVSNNDVGPGRSEEVFLQVQYAPEPSTVQILHSPAVEGSQVE
FLCMSLANPLPTNYTWYHNGKEMQGRTEEKVHI PKILPWHAGTYSVAENILGTGQRGPGAELDVQYPPK
KVTTVIQNPMPIREGDVTLSNYSNPNPSVTRYEWKPHGAWEEPGLGVLKIQNVGWDNTTIIACARCNSW
CSWASPVVALNVQYAPRDVVRVKIKPLSEIHSNNSVSLQCDFSSSHPKVEVQFFWEKNGRLLGKESQLNFD
ISPEDAGSYSCWVNSIGQTKAWTLEVLVYAPRRLRVSMSPGDQVMEGKSATLTCESDANPPVSHYTW
DWNQSLPHHSQKLRLPEVKVQHSWAYWCOGTNSVGKGRSLSTLTVYYSPETIGRRVAVGLGSCLA ILI
LAICGLKLQRRWKRTQSQQGLQENSSGQSFVRNKKVRRAPLSEGPSLGCYNPMMEDGISYTTLRFP

NIPRTGDAESSEMQRPPRTCDTDTVTYSALHKRQVGDYENVIPDFPEDEGIHYSELIQFGVGERPQAQENV
DYVILKH

<210> 62
<212> DNA
<213> Homo sapiens

<400> 62

62>CD79beta, old-SEQ-ID_504, partial cDNA

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gccaggggagcctgcaccaggtcatggggcgacctggctctcactcctggcctgggtgct
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<210> 63
<212> PRT
<213> Homo sapiens

<400> 63

63>CD79beta, old-SEQ-ID_1747, partial protein

LKQRNTLKDGIIMIQTLLIILFIIIVPIFLLLDKDDSKAGMEEDHTYEGLDIDQTATYEDI
VTLRTGEVKWSVGEHPQE

<210> 64
<212> DNA
<213> Homo sapiens

<400> 64

64>CD79beta, Old-SEQ-ID_5238, partial cDNA

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<210> 65
<212> DNA
<213> Homo sapiens

<400> 65

65>CD79beta, full-length cDNA

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<210> 66

<212> PRT
<213> Homo sapiens

<400> 66

66>CD79beta, full-length protein

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SGNVSWLWKQEMDENPQQLKLEKGRMEESQNESLATLTIQGIRFEDNGIYFCQKCNNTSEVYQGC
RVMGFSTLAQLKQRTNLKDGIMIQTLLIILFIIVPIFLLLDKDDSKAGMEEDHTYEGLDIDQTATY
VTLRTGEVKWSVGEHPGQE

<210> 67
<212> DNA
<213> Homo sapiens

<400> 67

67>Ly1450P, Old-SEQ-ID_6695, partial cDNA

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<210> 68
<212> DNA
<213> Homo sapiens

<400> 68

68>Ly1450P, partial cDNA

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<210> 69
<212> DNA
<213> Homo sapiens

<400> 69

69>Ly1451P, Old-SEQ-ID_3507, partial cDNA

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<210> 70

<212> DNA

<213> Homo sapiens

<400> 70

70>Ly1451P, partial cDNA

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71>Ly1451P, partial protein

MDSRGSPLGGLGLPCGASLRRTPASPSDAIQRALPGRKLPRWNASPEQRVAVPCGGLTQWLNTGKELALGVRTSETCLRG
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72>Ly1454P, Old-SEQ-ID_3577, partial cDNA

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73>Ly1454P, FLJ40597, full-length cDNA

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74>Lyl1454P, FLJ40597, full-length protein

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IIHVPGGKDV RKT VTSVLEECEQRKYTSVSLPAIGTGNAGKNPITVADNI IDAIVDFSSQHSPTSLKTVK
VVIFQPELLNIFYDSMKKRDLSASLNFQSTFSMTTCNLPEHWTDMNHQLFCMVQLEPGQSEYNTIKDKFT
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75>Lyl1485P, Old-SEQ-ID_2789, partial cDNA

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76>Lyl1485P, Old-SEQ-ID_2417, partial protein

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77>Lyl1485P, Old-SEQ-ID_10476, partial cDNA

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80>Ly1500P, splice-1 FLJ20706, full-length protein

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81>Ly1500P, splice-2 DKFZp667N1611, full-length cDNA

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82>Ly1500P, splice-2, DKFzP667N1611, full-length protein
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83>Ly1500P, splice-3, FLJ34204 fis, full-length cDNA
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84>Ly1500P, splice-3, FLJ34204 fis, full-length protein
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85>Ly1516P, Old-SEQ-ID_8949, partial cDNA
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86>Ly1516P, Similar to CD47 antigen, splice_form-1, full-length cDNA
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88>Ly1516P, cDNA DKFZp313F0317, splice_form-2, partial cDNA
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90>Ly1678P, Old-SEQ-ID_8607, partial cDNA

91>Ly1678P, splice_form_1a (shorter), partial cDNA

35/49.

tacagcttttaggtcttcagctgcccttctggcgagtagatgcacaggattgtaaatgagaaatgcagtcattttccagt
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92>Ly1678P, splice_form_1b (longer), partial cDNA

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93>Ly1678P, slice_form_2, partial cDNA

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94>Ly1680P, partial cDNA

aatcaaaagggtgggaggattttccctaaactgacttagcaggactcttggtacaattggactaggcagggtgaagacagga
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aaaa

95>Ly1686P, partial cDNA

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tatctgggagg

96>Ly1687P, partial cDNA

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97>Ly1706P, FLJ21578, partial cDNA

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gagtatattacaaaatgtaatgacttttgtacattactcttttttcttgcataaaaaaaaaaaaaaaaa

98>Ly1712P, partial cDNA

ccacaaaataagggtctaattcaataaattatagtaaatataatgtaataatattacatgccactaaaaagaataaggta
gctgtatatttcttggtatggaaaaacatattaatatgttataaaactattaggttgggtgcaaaactaattgtgggtttt
gccattgaaatggcattgaaataaaagtgtaaagaaatctataccagatgtagtaacagtggtttgggtctgggaggttg
gattacaggggagcatttgatttctatgttgngtatttctatantgtttgaattgtttagaatgaatctgtntt

99>Ly1729P, Old-SEQ-ID_6586, partial cDNA

ccagtatggaatccagaaggaccgagtgataagagcgctgtcggttcaatgaaatgga
ggccccgaccacagcttataagaagacgacgcccataagaagcgcttctagtgggccccg
tgggctgaaggcgaaatttgagtcctatggctgaggagaagaggaagcgagaggaagagga
gaaggcacagcaggtggccaggaggcaacaggagcgaaaggctgtgacaaagaggagccc
tgaggctccacagccagtgatagctatggaagagccagcagtagccgccccactgcccac
gaaatctcctcagagg

100>Ly1729P, hematopoietic cell-specific Lyn substrate 1 (HCLS1), full-length cDNA
aattccgccccgcttagaacagaggcttgacaggtggagatgtggaagtctgtagtgggcatgatg
tgtctgttttcgtggagacccagggtgatgattgggacacagatcctgactttgtgaatgacatctctga
aaaggagcaacgatggggagccaagaccatcgaggggtctggacgcacagaacacatcaacatccaccag
ctgaggaacaaagtatcagaggagcatgatgttctcaggaagaaagagatggagtccagggccaaagcat
cccatggctatggaggtcggtttggagtagaaagagaccgaatggacaagagtgcagtgggcatgagta
tgttgcgaggtggagaagcactctctcagacggatgctgccaaaggcttgggggcaagtacggaggt
gagagggacagggcagacaagtgcagcagtcggctttgattataaaggagaagtggagaagcatacatctc
agaagattactctcggtggctttgggtggccggtacggggtggagaaggataaatgggacaaagcagctct
gggatatgactacaagggagagacggagaaacacagatcccagagagattatgccaagggtttgggtggc
cagtatgggaatccagaaggcagtgataagagcgctgtcggttcaatgaaatggaggccccgacca
cagcttataagaagacgacgcccataagaagcgcttctagtgggtgcccgtgggtgaaggcgaaatttga
gtccatggctgaggagaagaggaagcgagaggaagaggagaaggcacagcaggtggccaggaggcaacag
gagcgaaaggctgtgacaaagaggagccctgagggtccacagccagtgatagctatggaagagccagcag
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gtctgagcctgtgagaaccagcaggggaacacccagtgcccttgctgccattaggcagactctcccgag
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agtacgtctagattgtgtggtttgctcattgtgctatttgccacttctctccctgaagaaatatctg
tgaaccttcttctgttcagtcctaaaattcgaaataaagtgagactatggttcacctgtaaaaaaaaaa
aagggaatt

101>Ly1729P, hematopoietic cell-specific Lyn substrate 1 (HCLS1), full-length protein

MWKSVMGHDVSVSVETQGGDWDTPDFVNDISEKEQRWGAKTIEGSGRTEHINIHQLRNKVSEEHDLVRK
KEMESGPKASHGYGGRFVERDRMDKSAVGHEYVAEVEKHSSQDAAGFGGKYGVERDRADKSAVGFDY
KGEVEKHTSQKDYSRGFGGRYGVKDKWDKALGYDYKGETEKHESQDYAKFGGQYGIQKDRVDKSAV
GFNEMEAPTAYKKTTPIEAASSGARGLKAKFESMAEEKRKEEEKAQQVARRQQRKAVTKRSPEAPQ
PVIAMEEPAPVAPLPKKISSEAWPPVGTTPPSSESEPVRTSREHPVPLLPPIRQTLPEDNEEPPALPPRTLE
GLQVEEFPVYAEPEPEPEPEPENDYEDVEEMDRHEQDEPEGDYEEVLEPEDSSFSSALAGSSGCPA
GAGAGAVALGISAVALYDQEGESDELSFDPDDVITDIEMVDEGWWRGRCHGHFGLFPANYVKLLE

102>Ly1848P, partial cDNA

ctgacagcatctggctttcagttcctcagtcaccactactttgtaccaaattcactgttttggtctgaaatctaatttt
gagtttagcaaggatg

103>Ly1859P, old-SEQ-ID_640, partial cDNA

ccagagtgagcagatacatcattggcaccaagggtctttttcaattcttggtcaatcctct
gcagcaagcaccctcgatgacgtcctcatagatgccctcagtggtcagagcctggctgc
ccacggcaaggacatccccctcgaactcaggcagctccttttgcagcctggctcgagtt
ggctcagcacaaaaggtaaaagatgcagagacccagcctcgatgaacctcctctgag
ccaacccgctgtccgatttgaatttcttcagcacgcgccccctgactctctccagcctct
gggcagcctggtcagagtgaggccgctgctcagacactggtcagccag

104>Ly1859P, old-SEQ-ID_2452, partial protein

LADQCLTTALNCDQAAQRLERVRGRVLKKFKSDSGLAQRFFIRGWGLCIFLPFVLSQLEP
GCKKELPEFEGDVLAVGSQALTTEGIYEDVIRGCLLQRIQDELKKTILGANDVSTL

105>Ly1859P, Old-SEQ-ID_3313, partial cDNA

ctgcaagacagcagagaanctgccaatatccagttagcagatgactttgctggcaagcag
aggaagnccggtaaaagcttgtctcccagccaggaaacttgacaccaagntaagatttgga
gctaggaaacaaacccaaaaggctcacagcaagcggagaaaaaaaccccaaatctgtaa
cctgtatcacaaagcgttcatactccttcagatataaagagttattagatatcaataagaa

aaatgcaaacactcctgaaaagtagaaaaagctatgaacaggcaattcactgaaattaa
aaaaaaaaaaaa

106>Lyl1859P, FLJ00140, full-length cDNA

cgcaggcgggtggtcgtggggaagggaagaggagccccgggagacgacagcagcatgggtgggcggccttc
gagccctctggacaagcagcagcggcagcacctaagggggtcagggtggacacctgctgaggaaacttcctg
ccttgctaccgtgggcagctggcagcgtctgtcctgcccagatctctcgagagctgggcccctcaggagc
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attacaggcatgagccaccgacccggcctgttattttaaataaaaaatatttaaaaataaagataaagg
aaactaaggcccaagcccgcccccaaccccacagctaatcaggccccagggttagggcagaagcctgtg
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ccgggttcaagcgatttctcctgcctcagcctcccgagtagctgggatttcaggcaccggccaccatgcct
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agcttgggcaatgtgttgaaacctgtctctactaaaaataaaataaaataaaataaaataaaataaaata
aataaaataaaataaaatttaaagaagctgggctgagatgggagatttgctgagcctgggaactcaaggc

41/49

110>Ly1867P, Old-SEQ-ID_3570, partial cDNA

aaaccttaagaaccacataataactatataatgcttttctgtacaaatctcaagaaacact
ttcatttcattaaacatcatgaaatccttaaatgtgttaaattggaaaaaatgaaacca
tgaacaaaaagctatacatgtaggtgcatatttatctcctcctgagttgggagaaatct
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aatatagacaaaaggtggtaaacaggtggttctcagagaagataaatacatgattatttaa
cataaaaagaaatgttcaatgtttctagaagacaaataattacaaacctaaacaataatgt
atatttgtagattggcataaattataataatccaacattgagttangtggaaataaataat
tggtaaaatatttctggaagacaatttgg

111>Ly1868P, partial cDNA

agaagtgattatgggattaaaagaatacataattacagtgttttgggattgggctcttttttttcttaatagaaaagcag
aaacttcataaataatagctgtgcttttagataaccagataacaaatattgtttcccctgaagatatgacctactagaacta
ctcacatatatagccaataattgctgacttaataggtatggtaaaatagctgataataagtcagactctcaagagtttc
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cacaacataatctgaaggagatcaaacatctgtaaggacaggtaccagtgatgataatatctgaaaacacaagccat
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cagcttggttctctctcactttttgtttctttttaatatgcaaa

112>Ly1886P, Old-SEQ-ID_6454

aaaaaaagacaatttgagcaggacgacctctccaatctgggtagcatggttagcctgtg
cagtaacaacgttaggcttgaggatgggtncaatgaaatgattctgattcggaaacgtt
ttgactttggactgtanaagcttttctttgatcacctgtgntggaggaaaggaaagaagc
ctt

113>Ly669S, intercellular adhesion molecule 3 (ICAM3), complete cDNA

cagctctctgtcagaatggccaccatggtaccatccgtgtgtgtggccaggcctgctggactctgctgg
tctgtgtgtgtgtgacccaggtgtccaggggcaggagttccttttgcgggtggagcccagaaccctgt
gctctctgtgtggaggtccctgtttgtgaactgcagtactgattgtcccagctctgagaaaaatcgccctg
gagacgtccctatcaaaggagctggtggccagtggtcatgggctgggcagccttcaatctcagcaacgtga
ctggcaacagctcggatcctctgtctcagtgtactgcaattggctcccagataacaggtcctctaacatcac
cgtgtacgggtcccgagcgtgtggagctggcaccctgcctccttggcagccggtggggccagaacttc
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114>Ly669S, intercellular adhesion molecule 3, complete protein

MATMVPVSLWPRACWTLVCCLLTPGVQGEFLLRVEPQNPNVLSAGGSLFVNCSTDPCSSEKIALETSL
KELVASGMGWAFFNLNVTGNRIILCSVYCNQSITGSSNITVYGLPERVELAPLPWPQPVGQNFTRLCO
VEGGSPTSLSLTVLLRWEEELSRQPAVEEPAEVTATVLASRDDHGAPFSCRTELDMPQGLGLFVNTSAP
ROLRTFVLVPTPPRLVAPRFLVETSWPVDCTLDGLFPASEAQVYLALGDQMLNATVMNHGDTLTATATA
TARADQEGAREIVCNVTLGGERREARENLTVFSFLGPIVNLSEPTAHEGSTVTVSCMAGARVQVTLTGVP
AAPGQPAQLQLNATESDDGRSFFCSATLEVDGEFLHRNSSVQLRVLYGPKIDRATCPQHLKWKDKTRHV
LQCQARGNPYPRLRCLKEGSSREVPVGI PFFVNVTHNGTYQCQASSSRGKYTLVVMDIEAGSSHFVFPV
VAVLLTLGVVTVIVLALMYVFREHQRSGSYHVREESTYLPPLTSMQPTTEAMGEEPSRAE

115>Ly672S, Old-SEQ-ID_3042, partial cDNA

cctgatgccgaatttcagtttggcacttacagcgaatctgagaggaaaaccgaggagta
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cgtcaacggggtctatgcctttggtttcctcttcatgctgccccagctctttgtgaacta
caagttgaagtcagtggcacatctgccctggaagg

116>Ly672S, cisplatin resistance related protein CRR9p, full-length cDNA
cagctccttcaccagcttgggtggtggcggtgttcgtggtctacgtggtgcacacctgctgggtcatgtac
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gcgggcaggggtgggagccctcacaggcaagggggcttggatttccatttcaggtggttttctaagt
ctccttatgtgaatttcaaacacgtatggaatttcattccgcatggactctgggatcaaaggctcttctct
cttttgtttg

117>Ly672S, cisplatin resistance related protein CRR9p, full-length protein
MWSGRSSFTSLVGVFVVVYVHTCWVYGVYTRPCSGDANCIPYLARRPKLQLSVYTTTRSHLGAENN
IDLVLNVEDFDVESKFERTVNVSVPKKTRNNGTLYAYIFLHHAGVLPWHDGKQVHLVSPLETTMVPKPEE
INLLTGESDQIEAEKKPTSALDEPVSHWRPRLALNVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYL
PILFIDQLSNRVKDLVINRSTTELPLTVSYDKVSLGRLRFVIMQDAVYSLQQFGFSEKDADEVKGI FV
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118>Ly675S, KIAA0906 gene, partial cDNA
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 gttctatgtgattttt

119>Ly675S, KIAA0906 protein, partial protein

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<210> 121

<211> 1270

<212> PRT

<213> Homo sapiens

<400> 121

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Met	Thr	Ser	Gly	Gly	Asp	Ala	Ala	Met	Phe	Arg	Asp	Gly	Lys	Glu	Pro
			20					25					30		
Gln	Pro	Ser	Ala	Glu	Ala	Ala	Ala	Ala	Pro	Ser	Leu	Ala	Asn	Ile	Ser
	35							40					45		

Cys	Phe	Thr	Gln	Lys	Leu	Val	Glu	Lys	Leu	Tyr	Ser	Gly	Met	Phe	Ser
50						55					60				
Ala	Asp	Pro	Arg	His	Ile	Leu	Leu	Phe	Ile	Leu	Glu	His	Ile	Met	Val
65					70					75					80
Val	Ile	Glu	Thr	Ala	Ser	Ser	Gln	Arg	Asp	Thr	Val	Leu	Ser	Thr	Leu
				85					90					95	
Tyr	Ser	Ser	Leu	Asn	Lys	Val	Ile	Leu	Tyr	Cys	Leu	Ser	Lys	Pro	Gln
			100					105					110		
Gln	Ser	Leu	Ser	Glu	Cys	Leu	Gly	Leu	Leu	Ser	Ile	Leu	Gly	Phe	Leu
		115					120					125			
Gln	Glu	His	Trp	Asp	Val	Val	Phe	Ala	Thr	Tyr	Asn	Ser	Asn	Ile	Ser
		130				135					140				
Phe	Leu	Leu	Cys	Leu	Met	His	Cys	Leu	Leu	Leu	Leu	Asn	Glu	Arg	Ser
145				150						155					160
Tyr	Pro	Glu	Gly	Phe	Gly	Leu	Glu	Pro	Lys	Pro	Arg	Met	Ser	Thr	Tyr
				165					170					175	
His	Gln	Val	Phe	Leu	Ser	Pro	Asn	Glu	Asp	Val	Lys	Glu	Lys	Arg	Glu
			180					185					190		
Asp	Leu	Pro	Ser	Leu	Ser	Asp	Val	Gln	His	Asn	Ile	Gln	Lys	Thr	Val
		195				200						205			
Gln	Thr	Leu	Trp	Gln	Gln	Leu	Val	Ala	Gln	Arg	Gln	Gln	Thr	Leu	Glu
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Asp	Ala	Phe	Lys	Ile	Asp	Leu	Ser	Val	Lys	Pro	Gly	Glu	Arg	Glu	Val
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Lys	Ile	Glu	Glu	Val	Thr	Pro	Leu	Trp	Glu	Glu	Thr	Met	Leu	Lys	Ala
				245					250					255	
Trp	Gln	His	Tyr	Leu	Ala	Ser	Glu	Lys	Lys	Ser	Leu	Ala	Ser	Arg	Ser
			260					265					270		
Asn	Val	Ala	His	His	Ser	Lys	Val	Thr	Leu	Trp	Ser	Gly	Ser	Leu	Ser
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Ser	Ala	Met	Lys	Leu	Met	Pro	Gly	Arg	Gln	Ala	Lys	Asp	Pro	Glu	Cys
		290				295					300				
Lys	Thr	Glu	Asp	Phe	Val	Ser	Cys	Ile	Glu	Asn	Tyr	Arg	Arg	Arg	Gly
305				310						315					320
Gln	Glu	Leu	Tyr	Ala	Ser	Leu	Tyr	Lys	Asp	His	Val	Gln	Arg	Arg	Lys
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Cys	Gly	Asn	Ile	Lys	Ala	Ala	Asn	Ala	Trp	Ala	Arg	Ile	Gln	Glu	Gln
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Leu	Phe	Gly	Glu	Leu	Gly	Leu	Trp	Ser	Gln	Gly	Glu	Glu	Thr	Lys	Pro
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Cys	Ser	Pro	Trp	Glu	Leu	Asp	Trp	Arg	Glu	Gly	Pro	Ala	Arg	Met	Arg
		370				375					380				
Lys	Arg	Ile	Lys	Arg	Leu	Ser	Pro	Leu	Glu	Ala	Leu	Ser	Ser	Gly	Arg
385				390						395					400
His	Lys	Glu	Ser	Gln	Asp	Lys	Asn	Asp	His	Ile	Ser	Gln	Thr	Asn	Ala
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Glu	Asn	Gln	Asp	Glu	Leu	Thr	Leu	Arg	Glu	Ala	Glu	Gly	Glu	Pro	Asp
			420					425					430		
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Glu	Ser	Leu	His	Ser	Glu	Asp	Phe	Leu	Glu	Leu	Cys	Arg	Glu	Arg	Gln
		450				455					460				
Val	Ile	Leu	Gln	Glu	Leu	Leu	Asp	Lys	Glu	Lys	Val	Thr	Gln	Lys	Phe
465				470						475					480
Ser	Leu	Val	Ile	Val	Gln	Gly	His	Leu	Val	Ser	Glu	Gly	Val	Leu	Leu
				485					490					495	
Phe	Gly	His	Gln	His	Phe	Tyr	Ile	Cys	Glu	Asn	Phe	Thr	Leu	Ser	Pro
			500					505					510		
Thr	Gly	Asp	Val	Tyr	Cys	Thr	Arg	His	Cys	Leu	Ser	Asn	Ile	Ser	Asp
		515					520					525			
Pro	Phe	Ile	Phe	Asn	Leu	Cys	Ser	Lys	Asp	Arg	Ser	Thr	Asp	His	Tyr
		530				535					540				
Ser	Cys	Gln	Cys	His	Ser	Tyr	Ala	Asp	Met	Arg	Glu	Leu	Arg	Gln	Ala
545				550						555					560
Arg	Phe	Leu	Leu	Gln	Asp	Ile	Ala	Leu	Glu	Ile	Phe	Phe	His	Asn	Gly
				565					570					575	
Tyr	Ser	Lys	Phe	Leu	Val	Phe	Tyr	Asn	Asn	Asp	Arg	Ser	Lys	Ala	Phe
			580					585						590	

Lys Ser Phe Cys Ser Phe Gln Pro Ser Leu Lys Gly Lys Ala Thr Ser.
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 Glu Asp Thr Leu Asn Leu Arg Arg Tyr Pro Gly Ser Asp Arg Ile Met
 610 615 620
 Leu Gln Lys Trp Gln Lys Arg Asp Ile Ser Asn Phe Glu Tyr Leu Met
 625 630 635 640
 Tyr Leu Asn Thr Ala Gly Arg Thr Cys Asn Asp Tyr Met Gln Tyr
 645 650 655
 Pro Val Phe Pro Trp Val Leu Ala Asp Tyr Thr Ser Glu Thr Leu Asn
 660 665 670
 Leu Ala Asn Pro Lys Ile Phe Arg Asp Leu Ser Lys Pro Met Gly Ala
 675 680 685
 Gln Thr Lys Glu Arg Lys Leu Lys Phe Ile Gln Arg Phe Lys Glu Val
 690 695 700
 Glu Lys Thr Glu Gly Asp Met Thr Val Gln Cys His Tyr Tyr Thr His
 705 710 715 720
 Tyr Ser Ser Ala Ile Val Ala Ser Tyr Leu Val Arg Met Pro Pro
 725 730 735
 Phe Thr Gln Ala Phe Cys Ala Leu Gln Gly Gly Ser Phe Asp Val Ala
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 Asp Arg Met Phe His Ser Val Lys Ser Thr Trp Glu Ser Ala Ser Arg
 755 760 765
 Glu Asn Met Ser Asp Val Arg Glu Leu Thr Pro Glu Phe Phe Tyr Leu
 770 775 780
 Pro Glu Phe Leu Thr Asn Cys Asn Gly Val Glu Phe Gly Cys Met Gln
 785 790 795 800
 Asp Gly Thr Val Leu Gly Asp Val Gln Leu Pro Pro Trp Ala Asp Gly
 805 810 815
 Asp Pro Arg Lys Phe Ile Ser Leu His Arg Lys Ala Leu Glu Ser Asp
 820 825 830
 Phe Val Ser Ala Asn Leu His His Trp Ile Asp Leu Ile Phe Gly Tyr
 835 840 845
 Lys Gln Gln Gly Pro Ala Ala Val Asp Ala Val Asn Ile Phe His Pro
 850 855 860
 Tyr Phe Tyr Gly Asp Arg Met Asp Leu Ser Ser Ile Thr Asp Pro Leu
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 Ile Lys Ser Thr Ile Leu Gly Phe Val Ser Asn Phe Gly Gln Val Pro
 885 890 895
 Lys Gln Leu Phe Thr Lys Pro His Pro Ala Arg Thr Ala Ala Gly Lys
 900 905 910
 Pro Leu Pro Gly Lys Asp Val Ser Thr Pro Val Ser Leu Pro Gly His
 915 920 925
 Pro Gln Pro Phe Phe Tyr Ser Leu Gln Ser Leu Arg Pro Ser Gln Val
 930 935 940
 Thr Val Lys Asp Met Tyr Leu Phe Ser Leu Gly Ser Glu Ser Pro Lys
 945 950 955 960
 Gly Ala Ile Gly His Ile Val Ser Thr Glu Lys Thr Ile Leu Ala Val
 965 970 975
 Glu Arg Asn Lys Val Leu Leu Pro Pro Leu Trp Asn Arg Thr Phe Ser
 980 985 990
 Trp Gly Phe Asp Asp Phe Ser Cys Cys Leu Gly Ser Tyr Gly Ser Asp
 995 1000 1005
 Lys Val Leu Met Thr Phe Glu Asn Leu Ala Ala Trp Gly Arg Cys Leu
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 Cys Ala Val Cys Pro Ser Pro Thr Thr Ile Val Thr Ser Gly Thr Ser
 1025 1030 1035 1040
 Thr Val Val Cys Val Trp Glu Leu Ser Met Thr Lys Gly Arg Pro Arg
 1045 1050 1055
 Gly Leu Arg Leu Arg Gln Ala Leu Tyr Gly His Thr Gln Ala Val Thr
 1060 1065 1070
 Cys Leu Ala Ala Ser Val Thr Phe Ser Leu Leu Val Ser Gly Ser Gln
 1075 1080 1085
 Asp Cys Thr Cys Ile Leu Trp Asp Leu Asp His Leu Thr His Val Thr
 1090 1095 1100
 Arg Leu Pro Ala His Arg Glu Gly Ile Ser Ala Ile Thr Ile Ser Asp
 1105 1110 1115 1120
 Val Ser Gly Thr Ile Val Ser Cys Ala Gly Ala His Leu Ser Leu Trp
 1125 1130 1135

Asn Val Asn Gly Gln Pro Leu Ala Ser Ile Thr Thr Ala Trp Gly Pro
 1140 1145 1150
 Glu Gly Ala Ile Thr Cys Cys Cys Leu Met Glu Gly Pro Ala Trp Asp
 1155 1160 1165
 Thr Ser Gln Ile Ile Ile Thr Gly Ser Gln Asp Gly Met Val Arg Val
 1170 1175 1180
 Trp Lys Thr Glu Asp Val Lys Met Ser Val Pro Gly Arg Pro Ala Gly
 1185 1190 1195 1200

Glu Glu Pro Leu Ala Gln Pro Pro Ser Pro Arg Gly His Lys Trp Glu
 1205 1210 1215
 Lys Asn Leu Ala Leu Ser Arg Glu Leu Asp Val Ser Ile Ala Leu Thr
 1220 1225 1230
 Gly Lys Pro Ser Lys Thr Ser Pro Ala Val Thr Ala Leu Ala Val Ser
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<210> 121
 <211> 647
 <212> PRT
 <213> Homo sapiens

<400> 121

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 35 40 45
 Asn Leu Ala Asn Pro Lys Ile Phe Arg Asp Leu Ser Lys Pro Met Gly
 50 55 60
 Ala Gln Thr Lys Glu Arg Lys Leu Lys Phe Ile Gln Arg Phe Lys Glu
 65 70 75 80
 Val Glu Lys Thr Glu Gly Asp Met Thr Val Gln Cys His Tyr Tyr Thr
 85 90 95
 His Tyr Ser Ser Ala Ile Ile Val Ala Ser Tyr Leu Val Arg Met Pro
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 Pro Phe Thr Gln Ala Phe Cys Ala Leu Gln Gly Gly Ser Phe Asp Val
 115 120 125
 Ala Asp Arg Met Phe His Ser Val Lys Ser Thr Trp Glu Ser Ala Ser
 130 135 140
 Arg Glu Asn Met Ser Asp Val Arg Glu Leu Thr Pro Glu Phe Phe Tyr
 145 150 155 160
 Leu Pro Glu Phe Leu Thr Asn Cys Asn Gly Val Glu Phe Gly Cys Met
 165 170 175
 Gln Asp Gly Thr Val Leu Gly Asp Val Gln Leu Pro Pro Trp Ala Asp
 180 185 190
 Gly Asp Pro Arg Lys Phe Ile Ser Leu His Arg Lys Ala Leu Glu Ser
 195 200 205
 Asp Phe Val Ser Ala Asn Leu His His Trp Ile Asp Leu Ile Phe Gly
 210 215 220
 Tyr Lys Gln Gln Gly Pro Ala Ala Val Asp Ala Val Asn Ile Phe His
 225 230 235 240
 Pro Tyr Phe Tyr Gly Asp Arg Met Asp Leu Ser Ser Ile Thr Asp Pro
 245 250 255
 Leu Ile Lys Ser Thr Ile Leu Gly Phe Val Ser Asn Phe Gly Gln Val
 260 265 270
 Pro Lys Gln Leu Phe Thr Lys Pro His Pro Ala Arg Thr Ala Ala Gly
 275 280 285
 Lys Pro Leu Pro Gly Lys Asp Val Ser Thr Pro Val Ser Leu Pro Gly
 290 295 300
 His Pro Gln Pro Phe Phe Tyr Ser Leu Gln Ser Leu Arg Pro Ser Gln
 305 310 315 320
 Val Thr Val Lys Asp Met Tyr Leu Phe Ser Leu Gly Ser Glu Ser Pro
 325 330 335

Lys Gly Ala Ile Gly His Ile Val Ser Thr Glu Lys Thr Ile Leu Ala
 340 345 350
 Val Glu Arg Asn Lys Val Leu Leu Pro Pro Leu Trp Asn Arg Thr Phe
 355 360 365
 Ser Trp Gly Phe Asp Asp Phe Ser Cys Cys Leu Gly Ser Tyr Gly Ser
 370 375 380
 Asp Lys Val Leu Met Thr Phe Glu Asn Leu Ala Ala Trp Gly Arg Cys
 385 390 395 400
 Leu Cys Ala Val Cys Pro Ser Pro Thr Thr Ile Val Thr Ser Gly Thr
 405 410 415
 Ser Thr Val Val Cys Val Trp Glu Leu Ser Met Thr Lys Gly Arg Pro
 420 425 430
 Arg Gly Leu Arg Leu Arg Gln Ala Leu Tyr Gly His Thr Gln Ala Val
 435 440 445
 Thr Cys Leu Ala Ala Ser Val Thr Phe Ser Leu Leu Val Ser Gly Ser
 450 455 460
 Gln Asp Cys Thr Cys Ile Leu Trp Asp Leu Asp His Leu Thr His Val
 465 470 475 480
 Thr Arg Leu Pro Ala His Arg Glu Gly Ile Ser Ala Ile Thr Ile Ser
 485 490 495
 Asp Val Ser Gly Thr Ile Val Ser Cys Ala Gly Ala His Leu Ser Leu
 500 505 510
 Trp Asn Val Asn Gly Gln Pro Leu Ala Ser Ile Thr Thr Ala Trp Gly
 515 520 525
 Pro Glu Gly Ala Ile Thr Cys Cys Cys Leu Met Glu Gly Pro Ala Trp
 530 535 540
 Asp Thr Ser Gln Ile Ile Thr Gly Ser Gln Asp Gly Met Val Arg
 545 550 555 560
 Val Trp Lys Thr Glu Asp Val Lys Met Ser Val Pro Gly Arg Pro Ala
 565 570 575
 Gly Glu Glu Pro Leu Ala Gln Pro Pro Ser Pro Arg Gly His Lys Trp
 580 585 590
 Glu Lys Asn Leu Ala Leu Ser Arg Glu Leu Asp Val Ser Ile Ala Leu
 595 600 605
 Thr Gly Lys Pro Ser Lys Thr Ser Pro Ala Val Thr Ala Leu Ala Val
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 Phe Cys Trp Ser Ala Asp Gly
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 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDM-797 PCR primer for His-Lyl452P

<400> 122
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32

<210> 123
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 <212> DNA
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 <223> PDM-799 PCR primer for His-Lyl452P

<400> 123
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35

<210> 124
 <211> 980
 <212> DNA
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human endogenous retroviral sequence (HERV)

<400> 124

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gccctgctcc	agtcacaccc	ggaagctgac	tggtccacgc	acagctgaag	catgaggaaa	660
ctcatcgcg	gactaatttt	ccttaaaatt	tagacttgca	cagtaaggac	ttcaactgac	720
cttcctcaga	ctgagaactg	tttccagtat	atacatcaag	tcactgaggt	aggacaaaag	780
attgctacat	tcctattatt	ttaaggttac	atthttgggg	acccctcttt	cttctgttct	840
agctattacc	tttcttgtgt	cacctagaaa	aggaccagtc	cttaattgta	ttttaaaaac	900
tgtgatcatg	ggaagcttta	aattggttca	ataacacgca	tcaagttggt	tatttcctgg	960
gctacatacc	ttggatagat					980

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